Amendments to the Specification

Please replace the paragraph beginning at page 1, line 2, with the following rewritten paragraph:

--CROSS REFERENCE TO RELATED APPLICATIONS

This application is divisional of U.S. Application No. 09/869,588, filed June 28, 2001, now U.S. Patent No. 6,790,657, which is a U.S. national stage of PCT/US00/00390 filed January 6, 2000, which was published in English under PCT Article 21(2), which in turn claims the benefit of U.S. Provisional Application No. 60/115,247, filed January 7, 1999.--

Please replace the paragraphs beginning at page 14, line 32, with the following rewritten paragraphs:

--The NCBI Basic Local Alignment Search Tool (BLAST) (Altschul et al. *J. Mol. Biol.* 215:403-10, 1990) is available from several sources, including the National Center for Biotechnology Information (NCBI, Bethesda, MD) and on the Internet, for use in connection with the sequence analysis programs blastp, blastn, blastx, tblastn and tblastx. ~~It can be accessed at http://www.ncbi.nlm.nih.gov/BLAST/.~~ A description of how to determine sequence identity using this program is also available on the Internet ~~at http://www.ncbi.nlm.nih.gov/BLAST/blast_help.html~~.

Homologs of the disclosed HIV and/or transgene proteins typically possess at least 60%, 70%, 75%, 80%, 90%, 95%, 98% or at least 99% sequence identity counted over full-length alignment with the amino acid sequence of the HIV and/or transgene protein using the NCBI Blast 2.0, gapped blastp set to default parameters. For comparisons of amino acid sequences of greater than about 30 amino acids, the Blast 2 sequences function is employed using the default BLOSUM62 matrix set to default parameters, (gap existence cost of 11, and a per residue gap cost of 1). When aligning short peptides (fewer than around 30 amino acids), the alignment should be performed using the Blast 2 sequences function, employing the PAM30 matrix set to default parameters (open gap 9, extension gap 1 penalties). Proteins with even greater similarity to the reference sequence will show increasing percentage identities when assessed by this method, such as at least 70%, 75%, 80%, 90%, 95%, 98%, or 99% sequence identity. When less than the entire sequence is being compared for sequence identity, homologs will typically

possess at least 75% sequence identity over short windows of 10-20 amino acids, and may possess sequence identities of at least 85% or at least 90% or 95% depending on their similarity to the reference sequence. Methods for determining sequence identity over such short windows are described on the Internet ~~at http://www.ncbi.nlm.nih.gov/BLAST/blast_FAQs.html.~~--

Please replace the paragraph beginning at page 20, line 24, with the following rewritten paragraph:

--A convenient and well-defined provirus that may be used for this purpose is the provirus molecular clone (pROD1), from HIV-2 ROD (the sequence of which is available under Genbank accession no. M15390, and is further described in Arya et al., *J. Acquir. Immune. Defic. Syndr.* 6:1205-1211, 1993; Arya et al., *J. Gen. Virol.* 75:2253-2260, 1994; and Arya et al., *Hum. Gene Ther.* 9:1371-1380, 1998). Other retroviral provirus constructs may also be used, for instance an HIV-1 or SIV provirus. The sequences for these proviruses are available on Genebank ~~at http://www.ncbi.nlm.nih.gov/Entrez/~~. Examples include, but are not limited to: Genbank Accession Nos. AF075702 (HIV-1 isolate SE8603 from Uganda), M17449 (HIV-1 isolate MN) and AF131870 (SIV). Such a provirus (or combination of complementary viruses), used to produce the packaging vector, should contain a substantially complete retroviral genome including the *gag*, *pol,* and *env* genes, a leader sequence and the 3' and 5' LTRs, and may contain the other HIV-2 structural genes shown in FIG. 2.--